



PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

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Limits Preview/Index History Clipboard Details

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Range: from to Features: ☐ SNP ☐ CDD ☒ MGC ☒ HPRD ☒

☐ 1: [CAF33259](#). Reports unnamed protein p...[gi:45112868]

[BLink](#), [Links](#)

LOCUS CAF33259 325 aa linear PLN 04-MAR-2004

DEFINITION unnamed protein product [Penicillium citrinum].

ACCESSION CAF33259

VERSION CAF33259.1 GI:45112868

DBSOURCE embl accession [CQ769141.1](#)

KEYWORDS .

SOURCE Penicillium citrinum

ORGANISM [Penicillium citrinum](#)

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.

REFERENCE 1

AUTHORS Asako,H. and Shimizu,M.

TITLE Modified reductase and its gene and use thereof

JOURNAL Patent: EP 1386961-A 04-FEB-2004;

Sumitomo Chemical Company, Limited (JP)

FEATURES Location/Qualifiers

source 1..325

/organism="Penicillium citrinum"

/db_xref="taxon:5077"

[Protein](#) 1..325

/name="unnamed protein product"

[CDS](#) 1..325

/coded_by="CQ769141.1:1..978"

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181 kfakvmphan qieihpflpn eelvqycfsk nimpvayspl gsqnqvpttg ervsenktln
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301 frfvnmkdtf gydvwpeeta knlsa

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Dec 2 2005 13:13:13

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Range: from to ☐ Reverse complemented strand Features: ☐

☐ 1: [CQ769141](#). Reports Sequence 2 from P...[gi:45112867] [Links](#)

LOCUS CQ769141 978 bp DNA linear PAT 04-MAR-2004

DEFINITION Sequence 2 from Patent EP1386961.

ACCESSION CQ769141

VERSION CQ769141.1 GI:45112867

KEYWORDS .

SOURCE *Penicillium citrinum*

ORGANISM *Penicillium citrinum*
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; *Penicillium*.

REFERENCE 1

AUTHORS Asako,H. and Shimizu,M.

TITLE Modified reductase and its gene and use thereof .

JOURNAL Patent: EP 1386961-A 2 04-FEB-2004;
Sumitomo Chemical Company, Limited (JP)

FEATURES

source Location/Qualifiers

1..978

/organism="Penicillium citrinum"

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CDS 1..978

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RKARSIGVSNWTIADLEKMSKFAKVMPHANQIEIHPFLPNEELVQYCFSKNIMPVAYS
PLGSQNQVPTTGERSVSENKTLNEIAEKGGNTLAQVLIAGLRRGVVLPKSSNPKRIE
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ORIGIN

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Dec 8 2005 13:13:13

Database : UniProt_05.80:*
 1: uniprot_sprot:*
 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1514	87.5	325	2	Q877A2_ASPOR	Q877a2 aspergillus
2	1477	85.3	325	2	Q4WQ65_ASPFU	Q4wq65 aspergillus
3	1471	85.0	325	2	Q5B1L7_EMENI	Q5b1l7 aspergillus
4	1471	85.0	325	2	Q7Z8L1_EMENI	Q7z8l1 emericella
5	1205.5	69.6	331	2	Q7S3U4_NEUCR	Q7s3u4 neurospora
6	1191	68.8	327	2	Q6RZX1_TRIAT	Q6rzx1 trichoderma
7	1137.5	65.7	323	2	Q51QM9_MAGGR	Q51qm9 magnaporthe
8	1038	60.0	256	2	Q4I4F0_GIBZE	Q4i4f0 gibberella
9	1037	59.9	254	2	O74646_GIBZE	O74646 gibberella
10	635	36.7	355	2	Q4PHK0_USTMA	Q4phk0 ustilago ma
11	623	36.0	1224	2	Q4P7C0_USTMA	Q4p7c0 ustilago ma
12	602.5	34.8	332	2	Q4IEY5_GIBZE	Q4iey5 gibberella
13	595.5	34.4	309	2	Q55SW0_CRYNE	Q55sw0 cryptococcu
14	593.5	34.3	309	2	Q5KH94_CRYNE	Q5kh94 cryptococcu
15	583	33.7	310	2	Q6FR42_CANGA	Q6fr42 candida gla
16	575.5	33.2	310	2	Q6FY54_CANGA	Q6fy54 candida gla
17	574.5	33.2	312	1	GCY_YEAST	P14065 saccharomyc
18	570.5	33.0	309	2	Q6CRC8_KLULA	Q6crc8 kluyveromyc
19	568	32.8	321	1	YDG7_SCHPO	Q10494 schizosacch
20	565.5	32.7	325	2	Q5KLM8_CRYNE	Q5klm8 cryptococcu
21	563.5	32.6	325	2	Q55YB1_CRYNE	Q55yb1 cryptococcu
22	560.5	32.4	313	2	Q4X1E8_ASPFU	Q4x1e8 aspergillus
23	559.5	32.3	322	1	ALDX_SPOSA	P27800 sporobolomy
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Database : A_Geneseq_21:*
 1: geneseqp1980s:*
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 5: geneseqp2002s:*
 6: geneseqp2003as:*
 7: geneseqp2003bs:*
 8: geneseqp2004s:*
 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	1731	100.0	325	5	ABB77965	Abb77965 Protein w
2	1731	100.0	325	7	ADE39629	Ade39629 Penicilli
3	1731	100.0	325	8	ADH44214	Adh44214 Penicilli
4	1731	100.0	325	8	ADL18258	Adl18258 Penicilli
5	1731	100.0	325	8	ADK70247	Adk70247 Penicilli
6	1731	100.0	325	8	ADM46686	Adm46686 325 amino
7	1731	100.0	325	8	ADM46567	Adm46567 Penicilli
8	1731	100.0	325	8	ADK51190	Adk51190 Wild-type
9	1731	100.0	325	8	ADN97092	Adn97092 3 hydroxy
10	1728	99.8	325	8	ADK51203	Adk51203 Mutant Pe
11	1726	99.7	325	8	ADK51204	Adk51204 Mutant Pe
12	1723	99.5	325	8	ADK51205	Adk51205 Mutant Pe
13	972.5	56.2	255	8	ADN20743	Adn20743 Bacterial
14	575.5	33.2	312	2	AAW29220	Aaw29220 S. cerevi
15	574.5	33.2	312	2	AAW29217	Aaw29217 S. cerevi
16	574.5	33.2	312	4	AAG63565	Aag63565 Amino aci
17	574.5	33.2	312	5	ABG93198	Abg93198 S. cerevi
18	574.5	33.2	312	8	ADS43942	Ads43942 Bacterial
19	574.5	33.2	313	4	AAG63566	Aag63566 Synthetic
20	573.5	33.1	312	2	AAW29218	Aaw29218 S. cerevi
21	568	32.8	321	8	ADN19632	Adn19632 Bacterial

*Not all
same in evs,
pen
had data*

RESULT 1

US-10-004-115B-1

; Sequence 1, Application US/10004115B

; Patent No. 6884607

; GENERAL INFORMATION:

; APPLICANT: ASAKO, HIROYUKI

; APPLICANT: MATSUMURA, KENJI

; APPLICANT: SHIMIZU, MASATOSHI

; APPLICANT: ITO, NOBUYA

; APPLICANT: WAKITA, RYUHEI

; TITLE OF INVENTION: PROCESS FOR PRODUCING OPTICALLY ACTIVE

; TITLE OF INVENTION: 4-HALO-3-HYDROXYBUTANOATE

; FILE REFERENCE: 7372-72249

; CURRENT APPLICATION NUMBER: US/10/004,115B

; CURRENT FILING DATE: 2001-12-06

; PRIOR APPLICATION NUMBER: JP 2000-372704

; PRIOR FILING DATE: 2000-12-07

; PRIOR APPLICATION NUMBER: JP 2001-006144

; PRIOR FILING DATE: 2001-01-15

; PRIOR APPLICATION NUMBER: JP 2001-026594

; PRIOR FILING DATE: 2001-02-02

; PRIOR APPLICATION NUMBER: JP 2001-175175

; PRIOR FILING DATE: 2001-06-11

; NUMBER OF SEQ ID NOS: 37

; SOFTWARE: PatentIn Ver. 3.2

; SEQ ID NO 1

; LENGTH: 325

; TYPE: PRT

; ORGANISM: Penicillium citrinum

US-10-004-115B-1

*Patent
DNA em 519
no variant*

Query Match 100.0%; Score 1731; DB 2; Length 325;

Best Local Similarity 100.0%; Pred. No. 3.3e-177;

Matches 325; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	61	EGIRDFLKENPSVKREDIFVCTKVWNHLHRYEDVLWSIDDSLKRLGLDYVDMFLVHWPIA	120
Qy	121	AEKNGQGEPKIGPDGKYVILKDLTENPEPTWRAMEKIYEDRKARSIGVSNWTIADLEKMS	180
Db	121	AEKNGQGEPKIGPDGKYVILKDLTENPEPTWRAMEKIYEDRKARSIGVSNWTIADLEKMS	180
Qy	181	KFAKVMPHANQIEIHPFLPNEELVQYCFSKNIMPVAYSPLGSQNQVPTTGERSVSENKTLN	240
Db	181	KFAKVMPHANQIEIHPFLPNEELVQYCFSKNIMPVAYSPLGSQNQVPTTGERSVSENKTLN	240
Qy	241	EIAEKGGNTLAQVLIAGLRRGYVVLKSSNPKRIESNFKSIELSDADFEAINAVAKGRH	300
Db	241	EIAEKGGNTLAQVLIAGLRRGYVVLKSSNPKRIESNFKSIELSDADFEAINAVAKGRH	300
Qy	301	FRFVNMKDTFGYDVWPEETAKNLSA	325

Db

301 FRFVNMKDTFGYDVWPEETAKNLSA 325

Database : PIR_80:*
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 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		Length	DB	ID	Description
		Match					
1	574.5	33.2		312	1	S22846	probable aldehyde
2	568	32.8		321	2	T38413	probable oxidoredu
3	559.5	32.3		323	2	S78113	aldehyde reductase
4	555	32.1		312	2	S61163	aldo-keto reductas
5	553	31.9		327	1	S76143	probable aldehyde
6	548.5	31.7		325	2	T39169	probable oxidoredu
7	547.5	31.6		344	1	S46020	probable aldehyde
8	529.5	30.6		309	2	A84599	hypothetical prote
9	529	30.6		290	2	T02543	aldehyde dehydroge
10	527.5	30.5		309	2	B84599	hypothetical prote
11	523.5	30.2		294	2	T02542	probable alcohol d
12	523.5	30.2		313	2	T09670	abscisic acid acti
13	521	30.1		320	2	T48188	aldose reductase-1
14	516	29.8		280	2	C98038	conserved hypothet
15	516	29.8		280	2	C95172	oxidoreductase, al
16	509	29.4		316	2	A37990	aldose reductase h
17	508.5	29.4		281	2	D86658	oxidoreductase ycg
18	503	29.1		276	2	C70040	plant-metabolite d
19	501.5	29.0		310	2	T17013	D-sorbitol-6-phosp
20	500	28.9		280	2	D69988	plant metabolite d
21	499.5	28.9		316	1	A60603	aldehyde reductase